

Amendment to the claims:

Please amend the claims as follows:

1. **(Currently amended)** A method for determining the presence of trait locus Rps8 in a soybean wherein the presence of trait locus Rps8 maps to soybean major linkage group F and is associated with soybean confers resistance to *Phytophthora sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, ~~and~~ 7 and combinations thereof, comprising:

analyzing genomic DNA from the soybean for the presence of ~~at least two a combination~~ of molecular markers on major linkage group F which are associated with ~~said~~ trait locus Rps8, whereby detecting the presence of the molecular markers provides an indication that ~~said~~ trait locus Rps8 is present in the soybean.

2. **(Currently amended)** The method of claim 1 wherein the ~~at least two~~ molecular markers are selected from the group consisting of Satt516, Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

3. **(Currently amended)** The method of claim 2 1 wherein the ~~at least two~~ molecular markers are markers Satt516 and Satt114 and wherein the method further comprises a step of determining that the soybean does not contain trait locus Rps3.

4. **(Withdrawn)** A method for introgressing soybean *Phytophthora sojae* resistance into non-resistant soybean germplasm or less resistant soybean germplasm comprising:

providing a first soybean germplasm which has Rps8-derived resistance to *Phytophthora sojae* and which has been selected by marker assisted selection using one or more nucleic acid markers, wherein the soybean *Phytophthora sojae* resistance is associated with the Rps8 gene that maps to soybean major linkage group F and wherein the molecular markers are associated with the Rps8 gene;

providing a second soybean germplasm which lacks Rps8-derived resistance to *Phytophthora sojae*;

crossing the first soybean germplasm with the second soybean germplasm to introgress the Rps8 gene into the genome of the second soybean germplasm to provide a hybrid introgressed germplasm having Rps8-derived resistance to *Phytophthora sojae*.

5. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is HFX01-602, or a descendant thereof.

6. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is OX-99128, or a descendant thereof.

7. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is OX-98317, or a descendant thereof.

8. **(Withdrawn)** The method of claim 4 wherein the first soybean germplasm is selected by a marker assisted selection technique selected from the group consisting of SSR analysis, RFLP analysis, RAPD analysis, and isozyme analysis.

9. **(Withdrawn)** The method of claim 4 wherein the nucleic acid markers are selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

10. **(Withdrawn)** A method for the production of a soybean cultivar adapted for conferring, in hybrid combination with a suitable second inbred, resistance to *Phytophthora sojae* comprising:

selecting a first donor parental line possessing the desired *Phytophthora sojae* resistance said first donor parental line comprising a *Phytophthora sojae* resistance gene Rps8 which is located on major linkage group F; crossing the first donor parental line with a second parental

line, which is high yielding in hybrid combination, to produce a segregating plant population of genetically heterogeneous plants;

screening the plants of the segregating plant population for the gene Rps8 by marker assisted selection using at least one associated markers;

selecting plants from the population having the gene Rps8; and

breeding by self crossing the plants containing the Rps8 gene until a line is obtained which is homozygous for resistance to *Phytophthora sojae* at Rps8 to give resistance to *Phytophthora sojae*.

11. **(Withdrawn)** The method of claim 10 wherein the at least one associated marker is selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

12. **(Withdrawn)** The method of claim 10 wherein the molecular markers are Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

13. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is HFX01-602, or a descendant thereof.

14. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is OX-99128, or a descendant thereof.

15. **(Withdrawn)** The method of claim 10 wherein the first donor parental line is OX-98317, or a descendant thereof.

16. **(Withdrawn)** The method of claim 10 wherein the plants of the segregating plant population are screened by a marker assisted selection technique selected the marker assisted selection comprises analyzing by a technique selected from the group consisting of, SSR analysis,.

17. **(Withdrawn)** A method for reliably and predictably introgressing soybean Rps8-derived resistance to *Phytophthora sojae* into susceptible soybean germplasm comprising analyzing soybean germplasm lines by marker assisted selection to identify those soybean germplasm lines having the Rps8 gene; and introgressing said Rps8 gene into said non-resistant soybean germplasm.

18. **(Withdrawn)** The method of claim 18 wherein markers for use in marker assisted selection are selected from the group consisting of. Satt595, Satt114, Satt334, Sat_317, Sat_197, Satt510, Satt335 and Satt144.

19. **(Withdrawn)** The method of claim 18 wherein the marker assisted selection comprises the use of SSR analysis.

20. **(Withdrawn)** A soybean plant produced according to the method of any one of claims 1-22.

21. **(Withdrawn)** A soybean plant having resistance to *Phytophthora sojae* comprising:

a soybean germplasm comprising an Rps8 gene

wherein the germplasm was produced by introgression of a soybean germplasm containing Rps8 in its genome with a soybean germplasm lacking the Rps8 gene in its genome.

22-24. **(Cancelled)**

25. **(Currently amended)** The method of claim 1, wherein the soybean is a progeny resulting from a cross between a first soybean parent having two parents wherein at least one parent has Rps8-associated derived *Phytophthora sojae* resistance and a second soybean parent that does not have Rps8-associated *Phytophthora sojae* resistance and wherein said parent is

identified by inoculation with one or more *P. sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7 or combinations thereof.

26. **(Currently amended)** The method of claim + 25, wherein ~~trait locus Rps8 is derived from the at least one parent that has Rps8 derived~~ *Phytophthora sojae* resistance is a soybean of plant line PI 399073 or a descendant thereof.

27. **(Currently amended)** A method of selecting a soybean plant having trait locus Rps8, comprising:

(a) ~~wherein the selecting a soybean plant that is a progeny from a cross between a first parent that has Rps8-associated derived~~ *Phytophthora sojae* resistance and a second parent that does not have Rps8-associated derived *Phytophthora sojae* resistance;[[.]] ~~the method comprising the steps of:~~

(b) ~~(a) detecting~~ a first nucleic acid from the first parent which is genetically linked to trait locus Rps8 wherein trait locus Rps8 is mapped to a locus on major linkage group F ~~and that~~ is located between molecular markers Satt114 and Satt516; and

(c) ~~(b) selecting the soybean plant progeny comprising the first nucleic acid thereby selecting the soybean plant having trait locus Rps8.~~

28. **(Currently amended)** The method of claim 27, wherein ~~trait locus Rps8~~ the first nucleic acid is ~~associated with a marker selected from the group consisting of:~~

(a) Satt 114, Satt 516, Satt595, Satt334, Sat_317, Sat_197, Satt510, Satt335, and Satt144;
and

(b) a marker linked to a marker of (a).

29. **(Currently amended)** The method of claim 27, wherein detecting the first nucleic acid comprises ~~RFLP, RAPD, AFLP, or~~ microsatellite analysis.

30. **(Previously presented)** The method of claim 27, wherein detecting the first nucleic acid comprises hybridization of a second nucleic acid to the first nucleic acid.

31. **(Currently amended)** The method of claim 27, wherein ~~trait locus Rps8 is derived from the first parent~~ is a soybean of plant line PI 399073 or a descendant thereof.

32. **(Currently amended)** The method of claim 27, wherein trait locus Rps8 is derived from the plant line HFX01-602 or a descendant thereof.

33. **(Currently amended)** A method of identifying soybean plants that are likely to have trait locus Rps8, the method comprising detecting a first locus on the genome of the plant which is genetically linked to trait locus Rps8, wherein the first locus maps to major linkage group F and is located between molecular marker Satt114 and Satt516, whereby detecting the first locus in the plant provides an indication that the trait locus Rps8 ~~resistance~~ is present in the plant.

34. **(Currently amended)** The method of claim 33, wherein the first locus is ~~associated with~~ linked to a marker selected from the group consisting of Satt595, Satt334, Sat_317, Sat_197, Satt510, Satt335, and Satt144.

35. **(Currently amended)** A method of selecting a soybean plant having Rps8-associated ~~derived~~ *Phytophthora sojae* resistance, comprising:

(a) ~~wherein the soybean plant is producing~~ a progeny from a cross between a first parent that has Rps8-associated ~~derived~~ *Phytophthora sojae* resistance and a second parent that does not have Rps8-associated ~~derived~~ *Phytophthora sojae* resistance; ~~[[.]] the method comprising the steps of:~~

(b) ~~(a)~~ detecting a *Phytophthora sojae* isolate that the second parent is susceptible to, wherein said *Phytophthora sojae* isolate is selected from the group consisting of pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, and combinations thereof; and

(c) ~~(b)~~ selecting the progeny that is resistant to said *Phytophthora sojae* isolate, thereby selecting a soybean plant having Rps8- ~~associated~~ derived *Phytophthora sojae* resistance.

36. **(Currently amended)** The method of claim 35, wherein the *Phytophthora sojae* isolate is selected from the group consisting of *P. sojae* ~~OH~~-race 1, ~~OH~~ race 4, ~~OH~~ race 17, ~~OH~~ race 25, ~~OH~~ race 30, and combinations thereof.

37. **(New)** The method of claim 35, wherein trait the first parent is a plant variety selected from the group consisting of HFX01-602, OX-98317, OX-99218, OX-99128 or descendants thereof.

38. **(New)** The method of claim 27, wherein the first parent is a plant variety selected from the group consisting of OX-98317, OX-99218, OX-99128 or descendants thereof.

39. **(New)** The method of claim 27, wherein the Rps8 derived *Phytophthora sojae* resistance of the first parent is determined by inoculation of the first parent with one or more *P. sojae* pathotypes selected from the group consisting of pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, and combinations thereof.

40. **(New)** The method of claim 25, wherein the at least one parent that has Rps8 derived *Phytophthora sojae* resistance is a plant variety selected from the group consisting of HFX01-602, OX-98317, OX-99218, OX-99128 or descendants thereof.

41. **(New)** A trait locus Rps8, wherein said trait locus Rps8 confers soybean resistance to *Phytophthora sojae* pathotypes vir1a, 1b, 1c, 1d, 1k, 2, 3a, 3b, 3c, 4, 5, 6, 7, and all combinations thereof, and wherein said trait locus maps to a region of soybean major linkage

group F that is flanked by molecular marker Satt516 and a molecular marker selected from the group consisting of Satt114, Satt334, Sat_317, Satt335, Satt510, Satt144 and Sat_197.